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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:16:38 ; Search time 91.75 seconds

(without alignments)  
15.135 Million cell updates/sec

Title: US-09-331-631A-3\_COPY\_74\_116

Perfect score: 250  
Sequence: 1 NDDPQTDCQCCQRRCRQEE.....RQDQYCCRCCKEICEEEEEEY 43

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	40.0	588	1 VCLB_GOSHI	P09801 gossypium h
2	90	36.0	605	1 VCLB_GOSHI	P09799 gossypium h
3	75	30.0	47	1 AGRP_LURCY	P56568 Iulita cylin
4	75	30.0	154	1 YS51_CAEEL	Q09662 caenorhabd
5	63.5	25.4	33	1 MBP1_MAIZE	P28794 zea mays (m
6	63.5	25.4	284	1 TPML_MOUSE	P46901 mus musculu
7	61.5	24.6	50	1 HSP1_MOUSE	P02319 mus musculu
8	61.5	24.6	50	1 HSP1_MOUSE	P10118 rattus norv
9	61	24.4	919	1 ANDR_HUMAN	P10275 homo sapien
10	60	24.0	907	1 ANDR_HUMAN	P10275 homo sapien
11	60	24.0	911	1 ANDR_PANTR	O91790 canis fami
12	59	23.6	2318	1 NTC3_MOUSE	O91775 pan troglod
13	58	23.2	445	1 NTR3_MOUSE	O61982 mus musculu
14	58	23.2	447	1 NTR3_MOUSE	O920V9 mus musculu
15	58	23.2	448	1 NTR3_MOUSE	O13133 homo sapien
16	57.5	23.0	217	1 KAPC_DICDI	P34099 dictyostell
17	57.5	23.0	284	1 KSI_HYDAT	P38978 hydra atlen
18	57.5	23.0	284	1 TPML_RAT	P06395 rattus norv
19	57.5	23.0	284	1 TPML_RAT	P06468 homo sapien
20	57.5	23.0	284	1 TPMB_HUMAN	P07951 homo sapien
21	57.5	23.0	284	1 TPMB_HUMAN	P02560 oryctolagus
22	57	22.8	217	1 YOM6_HUMAN	P00533 homo sapien
23	57	22.8	223	1 CAS2_SHEEP	P30652 caenorhabd
24	57	22.8	1166	1 XMRK_XIPMA	P04654 ovis aries
25	56.5	22.6	284	1 TPML_CHICK	P13388 xiphophoru
26	56.5	22.6	284	1 TPMB_CHICK	P04267 gallus gall
27	56.5	22.6	1407	1 TRHY_RABIT	P13352 gallus gall
28	56	22.4	210	1 YOEI_ECOLI	P37709 oryctolagus
29	56	22.4	251	1 GDBX_WHEAT	Q46941 escherichia
30	56	22.4	302	1 GDBX_WHEAT	P08079 triticum ae
31	56	22.4	327	1 GDBX_WHEAT	P21292 triticum ae
32	56	22.4	1210	1 EGFR_WHEAT	P08453 triticum ae
33	55.5	22.2	639	1 GLCX_SOYBN	O01279 mus musculu
					P11827 glycine max

34	55.5	22.2	968	1 CC28_SCHPO	Q10752 schizosacch
35	54.5	21.8	338	1 FSA_HUMAN	P19883 homo sapien
36	54	21.6	223	1 CAS2_CAPHI	P33049 capra hircu
37	54	21.6	258	1 ZSS_RICCO	P01089 ricinus com
38	54	21.6	285	1 INVQ_CANFA	P18174 canis fami
39	54	21.6	577	1 MTG8_MOUSE	O61909 mus musculu
40	54	21.6	604	1 MTG8_HUMAN	Q06455 homo sapien
41	54	21.6	626	1 AH12_ARAHY	P43238 arachis hyp
42	54	21.6	758	1 YM38_YEAST	Q03825 saccharomyc
43	54	21.6	1339	1 ERB3_RAT	O62799 rattus norv
44	54	21.6	1403	1 PRO_DROME	P29617 drosophila
45	53.5	21.4	49	1 HSP1_PIG	P04101 sus scrofa

## ALIGNMENTS

RESULT 1	VCLB_GOSHI	STANDARD;	PRT;	588 AA.
ID	P09801;			
AC	01-MAR-1989 (Rel. 10, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).			
OS	Gossypium hirsutum (Upland cotton).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Malvales; Malvaceae; Gossypium.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Chlan C.A., Pyle J.B., Legocki A.B., Dure L. III;			
RT	"Developmental biochemistry of cottonseed embryogenesis and germination. XVII. cDNA and amino acid sequences of the members of the storage protein families."			
RT	Plant Mol. Biol. 7:475-489(1986).			
CC	- FUNCTION: SEED STORAGE PROTEIN.			
CC	- SUBCELLULAR LOCATION: CYTOPLASMIC MEMBRANE-BOUND VACUOLAR PROTEIN BODIES.			
CC	- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICTILIN, CONGLICININ, ETC.).			
CC	THIS SWISS-PROT ENTRY IS COPYRIGHTED BY THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION - THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL ENTITIES REQUIRES A LICENSE AGREEMENT (SEE <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> OR SEND AN EMAIL TO <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	EMBL: M16891; AAA33071.1; -			
DR	PIR: A30838; FMCNAB.			
DR	HSSP: P50477; ICAX.			
DR	INTERPRO: IPR001113; -			
DR	PFAM: PF00546; Seedstore-7s; 1.			
KW	Seed storage protein; Signal.			
FT	SIGNAL 1			
FT	CHAIN 26			
FT	SEQUENCE 588 AA; 69729 MW; 635699B29A8B8ADB CRC64;			
Query Match	40.0%; Score 100; DB 1; Length 588;			
Best Local Similarity	45.0%; Pred. No. 0.00074;			
Matches	18; Conservative 10; Mismatches 10; Indels 2; Gaps 1;			
OY	3 DDPTDCCQCCQRRCRQESGPRQDYCCQRRCKEICEEEEEE 42			
DB	81 EDPPRRYECCQCCQRRCRQEE--RQPPCCQCCQRRCKEICEEEEEE 118			
RESULT 2	VCLB_GOSHI	STANDARD;	PRT;	605 AA.
ID	P09801;			

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AC P09799;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Malvales; Malvaceae; Gossypium.
RN [1]
RP SEQUENCE FROM N.A.
RA Chian C.A., Borroto K., Kamalay J.A., Dure L. III;
RT "Developmental biochemistry of cottonseed embryogenesis and
RT germination. XIX. Sequences and genomic organization of the alpha
RT globulin (vicilin) genes of cottonseed.";
RL Plant Mol. Biol. 9:533-546(1987).
CC -1- FUNCTION: SEED STORAGE PROTEIN.
CC -1- SUBCELLULAR LOCATION: CYTOLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
CC BODIES.
CC -1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CC CONVICILIN, CONGLYCININ, ETC.).
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CC -----
CC EMBL, M19378; AAA33069.1; -.
CC PIR, S06398; S06398.
CC DR HSSP; P50477; ICAX.
CC DR INTERPRO: IPR001113; -.
CC DR PFMAM: PF00546; Seedstore 7s; 1.
CC KW Seed storage protein; Signal.
CC FT SIGNAL 1 23
CC FT CHAIN 24 605 VICILIN GC72-A.
CC SQ SEQUENCE 605 AA; 71049 MW; C9DB9371C976953B CRC64;

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Query Match 36.0%; Score 90; DB 1; Length 605;
Best Local Similarity 35.9%; Pred. No. 0.0085;
Matches 14; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
Oy 2 QDDPOTDCOCRCRQESGPRQOQYCORCKEICEE 40
Db 115 QQQPDKRKECCQRCQWQEQRPKRQCKVKECRQYQED 153

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RESULT 3
AGRP_LUFCY STANDARD: PRT: 47 AA.
ID AGRP_LUFCY
AC P56568;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 6.5 KDA ARGININE/GLUTAMATE-RICH POLYPEPTIDE (6.5K-AGRP).
OS Luffa cylindrica (Smooth loofah) (Sponge gourd).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Cucurbitales; Cucurbitaceae; Luffa.
RN [1]
RP SEQUENCE.
RA Kimura M., Park S.S., Sakai R., Yamasaki N., Funatsu G.;
RT "Primary structure of 6.5k-arginine/glutamate-rich polypeptide from
RT the seeds of sponge gourd (Luffa cylindrica).";
RL Biosci. Biotechnol. Biochem. 61:984-988(1997).
CC -1- FUNCTION: STORAGE PROTEIN WHICH PROVIDES NITROGEN AND CARBON
CC RESERVES DURING GERMINATION AND SEEDLING GROWTH.
CC -1- MASS SPECTROMETRY: MW=5693.39; METHOD=MALDI.

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CC -1- SIMILARITY: SOME, TO 7S SEED STORAGE PROTEINS.
CC KW Seed storage protein.
CC FT DISULFID 12 33
CC FT DISULFID 16 29
CC SQ SEQUENCE 47 AA; 5698 MW; 588BDECB2273AC05 CRC64;

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Query Match 30.0%; Score 75; DB 1; Length 47;
Best Local Similarity 37.1%; Pred. No. 0.041;
Matches 13; Conservative 10; Mismatches 8; Indels 4; Gaps 1;

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Oy 5 POTDCOCRCRCRQESGPRQOQYCORCKEICEE 39
Db 5 PRTEYACRVRQCVAEHGVET---QRRCQGVCEK 35

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RESULT 4
Y551_CAEEL STANDARD: PRT: 154 AA.
ID Y551_CAEEL
AC Q09662;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HYPOHETICAL 15.6 KDA PROTEIN ZK673.1 IN CHROMOSOME II PRECURSOR.
GN ZK673.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CC [1]
CC -1- SIMILARITY: STRONG, TO C.ELEGANS E04D5.4 AND SOME, TO C.ELEGANS
CC C03G6.13.
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CC -----
CC EMBL, Z48585; CAA8486.1; -.
CC DR HSSP; P01551; IACX.
CC DR WORMPEP: ZK673.1; CE16742.
CC KW Hypothetical protein; Signal.
CC FT SIGNAL 1 19
CC FT CHAIN 20 154 HYPOTHETICAL PROTEIN ZK673.1.
CC SQ SEQUENCE 154 AA; 15637 MW; 323A02CA3A2E782AB CRC64;

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Query Match 30.0%; Score 75; DB 1; Length 154;
Best Local Similarity 41.9%; Pred. No. 0.11;
Matches 13; Conservative 3; Mismatches 15; Indels 0; Gaps 0;

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Oy 3 DDPOTDCOCRCRQESGPRQOQYCORCKEICEE 33
Db 69 DDPNTDCTQYSLCSNAKYTPLLQDFCKTC 99

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RESULT 5
MBPL_MAIZE STANDARD: PRT: 33 AA.
ID MBPL_MAIZE
AC P28794;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)

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DR EMBL: X14003; CAA32169.1; -
DR EMBL: M27500; AAA39985.1; -
DR EMBL: 247352; CAA87410.1; -
DR PIR: A02660; HSMSS1.
DR PIR: S03820; S03820.
DR PIR: A28331; A28331.
DR MGI: 97765; PRM1.
DR INTERPRO: IPR000221; -.
DR PIR: PF00260; Protamine_P1.1.
DR PROSITE: PS00048; Protamine_P1.1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KM Testis; DNA condensation; Nuclear protein.
FT INIT_MET 0 0
FT DISULFID 5 5 INTERCHAIN (WITH CYS-21) (BY SIMILARITY).
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 21 21 INTERCHAIN (WITH CYS-5) (BY SIMILARITY).
FT DISULFID 36 36 INTERCHAIN (WITH CYS-36) (BY SIMILARITY).
FT DISULFID 37 47 BY SIMILARITY.
SQ SEQUENCE 50 AA: 6827 MW: B61CAF3D1BBF4978 CRC64:

Query Match          24.6% Score 61.5; DB 1; Length 50;
Best Local Similarity 31.4%; Pred. No. 1.1;
Matches 11: Conservative 9; Mismatches 10; Indels 5; Gaps 1;

QY 9 COQCQRCHQDESPPROQYCCRCCKEICEEEY 43
   1:::||||: ||::|:|:| 1
DB 14 CRRRRRCRR-----RRRCRRRRRRRCRRRSY 43

RESULT 8
HSP1_RAT
ID HSP1_RAT STANDARD; PRT; 50 AA.
AC P10118;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Sperm protamine P1 (CYSTEINE-RICH PROTAmine).
GN PRM1 OR PRM-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89335257; PubMed=2757789;
RA Klemm U., Lee C.H., Burfield P., Hake S., Engel W.;
RT "Nucleotide sequence of a cDNA encoding rat protamine and the haploid
RL expression of the gene during rat spermatogenesis.";
RL Biol. Chem. Hoppe-Seyler 370:293-301(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96341725; PubMed=8720108;
RA Schueter G., Celik A., Obata R., Schlicker M., Hofferbert S.,
RA Schlung A., Adham I.M., Engel W.;
RT "Sequence analysis of the conserved protamine gene cluster shows that
RT it contains a fourth expressed gene.";
RL Mol. Reprod. Dev. 43:1-6(1996).
RN [3]
RP SEQUENCE.
RX MEDLINE=89207111; PubMed=3072011;
RA Ammer H., Henschen A.;
RT "Rat sperm protamine. Isolation and sequence analysis.";
RL Biol. Chem. Hoppe-Seyler 369:1301-1306(1988).
RN [4]
RP SEQUENCE OF 1-15 AND 44-50.
RX MEDLINE=76184789; PubMed=1268226;
RA Kistler W.S., Keim P.S., Hennikson R.L.;
RT "Partial structural analysis of the basic chromosomal protein of rat
RT spermatozoa.";
RL Biochim. Biophys. Acta 427:752-757(1976).
CC -I- FUNCTION: PROTAminES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

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CC -I- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
CC DNA-HELIX (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: NUCLEAR.
CC -I- TISSUE SPECIFICITY: TESTIS.
CC -----
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CC -----
DR EMBL: 246939; CAA87061.1; -
DR PIR: A27128; A27128.
DR PIR: S03997; S03997.
DR INTERPRO: IPR000221; -.
DR PIR: PF00260; Protamine_P1.1.
DR PROSITE: PS00048; Protamine_P1.1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KM Testis; DNA condensation; Nuclear protein.
FT INIT_MET 0 0
FT DISULFID 5 5 INTERCHAIN (WITH CYS-21) (BY SIMILARITY).
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 21 21 INTERCHAIN (WITH CYS-5) (BY SIMILARITY).
FT DISULFID 36 36 INTERCHAIN (WITH CYS-36) (BY SIMILARITY).
FT DISULFID 37 47 BY SIMILARITY.
SQ SEQUENCE 50 AA: 6889 MW: B60B9F3D1BB6D978 CRC64:

Query Match          24.6% Score 61.5; DB 1; Length 50;
Best Local Similarity 31.4%; Pred. No. 1.1;
Matches 11: Conservative 9; Mismatches 10; Indels 5; Gaps 1;

QY 9 COQCQRCHQDESPPROQYCCRCCKEICEEEY 43
   1:::||||: ||::|:|:| 1
DB 14 CRRRRRCRR-----RRRCRRRRRRRCRRRSY 43

RESULT 9
ANDR_HUMAN
ID ANDR_HUMAN STANDARD; PRT; 919 AA.
AC P10275;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
GN AR OR NR3C4 OR DHTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89112208; PubMed=3216866;
RA Lubahn D.B., Joseph D.R., Sar M., Tan J., Higgs H.N., Larson R.E.,
RA French F.S., Wilson E.M.;
RT "The human androgen receptor: complementary deoxyribonucleic acid
RT cloning, sequence analysis and gene expression in prostate.";
RL Mol. Endocrinol. 2:1265-1275(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90083302; PubMed=2594783;
RA Lubahn D.B., Brown T.R., Simental J.A., Higgs H.N., Migeon C.J.,
RA Wilson E.M., French F.S.;
RT "Sequence of the intron/exon junctions of the coding region of the
RT human androgen receptor gene and identification of a point mutation
RT in a family with complete androgen insensitivity.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9534-9538(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90258935; PubMed=2342476;
RA Govindan M.V.;
RT "Specific region in hormone binding domain is essential for hormone

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RT binding and trans-activation by human androgen receptor.";  
 RL Mol. Endocrinol. 4:417-427(1990).  
 [4]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=PROSTATE;  
 RX MEDLINE=89017168; PubMed=2174628;  
 RA Chang C., Kokontis J., Liao S.;  
 RT "Structural analysis of complementary DNA and amino acid sequences of  
 human and rat androgen receptors.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7211-7215(1988).  
 [5]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=PROSTATE;  
 RX MEDLINE=89098909; PubMed=2911578;  
 RA Tilley W.D., Marceli M., Wilson J.D., McPhaul M.J.;  
 RT "Characterization and expression of a cDNA encoding the human androgen  
 receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:327-331(1989).  
 [6]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=PROSTATE;  
 RX MEDLINE=91155943; PubMed=2293020;  
 RA Marceli M., Tilley W.D., Wilson C.M., Griffin J.E., Wilson J.D.,  
 McPhaul M.J.;  
 RT "Definition of the human androgen receptor gene structure permits the  
 identification of mutations that cause androgen resistance: premature  
 termination of the receptor protein at amino acid residue 588 causes  
 complete androgen resistance.";  
 RL Mol. Endocrinol. 4:1105-1116(1990).  
 [7]  
 RN SEQUENCE OF 189-919 FROM N.A.  
 RX MEDLINE=88178111; PubMed=3353726;  
 RA Chang C., Kokontis J., Liao S.;  
 RT "Molecular cloning of human and rat complementary DNA encoding  
 androgen receptors.";  
 RL Science 240:324-326(1988).  
 [8]  
 RN SEQUENCE OF 468-919 FROM N.A.  
 RX MEDLINE=88240407; PubMed=337788;  
 RA Trapman J., Klaassen P., Kuiper G.G.J.M., van der Kooij J.A.G.M.,  
 Faber P.W., van Rooij H.C.J., Geurts van Kessel A., Voorhorst M.M.,  
 Mulder E., Brinkmann A.O.;  
 RT "Cloning, structure and expression of a cDNA encoding the human  
 androgen receptor.";  
 RL Biochem. Biophys. Res. Commun. 153:241-248(1988).  
 [9]  
 RN POLYMORPHISM OF POLY-GLN REGION.  
 RX MEDLINE=92220629; PubMed=1561105;  
 RA Stedens H.F., Oostera B.A., Brinkmann A.O., Trapman J.;  
 RT "Trinucleotide repeat polymorphism in the androgen receptor gene  
 (AR).";  
 RL Nucleic Acids Res. 20:1427-1427(1992).  
 [10]  
 RN POLYMORPHISM OF POLY-GLY REGION.  
 RX TISSUE=BL00D;  
 RA Lu J., Danielsen M.;  
 RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 [11]  
 RN VARIANTS SBMA IN POLY-GLN REGION.  
 RX MEDLINE=91287825; PubMed=2062380;  
 RA Spada A.R., Wilson E.M., Lubahn D.B., Harding A.E., Fischback K.H.;  
 RT "Androgen receptor gene mutations in X-linked spinal and bulbar  
 muscular atrophy.";  
 RL Nature 352:77-79(1991).  
 [12]  
 RN REVIEW ON VARIANTS.  
 RX MEDLINE=95023089; PubMed=7937057;  
 RA Patterson M.N., Hughes L.A., Gottlieb B., Pinsky L.;  
 RT "The androgen receptor gene mutations database.";  
 RL Nucleic Acids Res. 22:3560-3562(1994).  
 [13]  
 RN REVIEW ON VARIANTS.  
 RX MEDLINE=97169385; PubMed=90165528;

RA Gottlieb B., Trifiro M., Lumbroso R., Vasilion D.M., Pinsky L.;  
 RT "The androgen receptor gene mutations database.";  
 RL Nucleic Acids Res. 25:158-162(1997).  
 [14]  
 RN VARIANT LNCAP ALA-877.  
 RX MEDLINE=91083633; PubMed=2260966;  
 RA Veldechoite J., Ris-Stalpers C., Kuiper G.G., Jenster G.,  
 Baerivoets C., Klaassen E., van Rooij H.C.J., Trapman J.,  
 Brinkmann A.O., Mulder E.;  
 RT "A mutation in the ligand binding domain of the androgen receptor of  
 human LNCap cells affects steroid binding characteristics and  
 response to anti-androgens.";  
 RL Biochem. Biophys. Res. Commun. 173:534-540(1990).  
 [15]  
 RN VARIANT CAIS MET-866.  
 RX MEDLINE=91186983; PubMed=2082179;  
 RA Brown T.R., Lubahn D.B., Wilson E.M., French F.S., Migeon C.J.,  
 Corlen J.L.;  
 RT "Functional characterization of naturally occurring mutant androgen  
 receptors from subjects with complete androgen insensitivity.";  
 RL Mol. Endocrinol. 4:1759-1772(1990).  
 [16]  
 RN VARIANT CYS-774.  
 RX MEDLINE=91310758; PubMed=1856263;  
 RA Marceli M., Tilley W.D., Zoppi S., Griffin J.E., Wilson J.D.,  
 McPhaul M.J.;  
 RT "Androgen resistance associated with a mutation of the androgen  
 receptor at amino acid 772 (Arg-->Cys) results from a combination of  
 decreased messenger ribonucleic acid levels and impairment of  
 receptor function.";  
 RL J. Clin. Endocrinol. Metab. 73:318-325(1991).  
 [17]  
 RN VARIANT CAIS ASN-695 AND HIS-695, AND SEQUENCE OF 629-723 FROM N.A.  
 RX MEDLINE=92131007; PubMed=1775137;  
 RA Ris-Stalpers C., Trifiro M.A., Kuiper G.G., Jenster G., Romalo G.,  
 Sai T., van Rooij H.C., Kautman M., Rosenfield R.L., Liao S.;  
 RT "Substitution of aspartic acid-686 by histidine or asparagine in the  
 human androgen receptor leads to a functionally inactive protein with  
 altered hormone-binding characteristics.";  
 RL Mol. Endocrinol. 5:1562-1569(1991).  
 [18]  
 RN VARIANTS CAIS AND PAIS.  
 RX MEDLINE=93338440; PubMed=1307250;  
 RA Batch J.A., Williams D.M., Davies H.R., Brown B.D., Evans B.A.J.,  
 Hughes I.A., Patterson M.N.;  
 RT "Androgen receptor gene mutations identified by SSCP in fourteen  
 subjects with androgen insensitivity syndrome.";  
 RL Hum. Mol. Genet. 1:497-503(1992).  
 [19]  
 RN VARIANT CAIS VAL-787.  
 RX MEDLINE=92235226; PubMed=1569163;  
 RA Nakao R., Hajl M., Yanase T., Ogo A., Takayanagi R., Katsube T.,  
 Fukumaki Y., Nawata H.;  
 RT "A single amino acid substitution (Met-786-->Val) in the steroid-  
 binding domain of human androgen receptor leads to complete androgen  
 insensitivity syndrome.";  
 RL J. Clin. Endocrinol. Metab. 74:1152-1157(1992).  
 [20]  
 RN VARIANT LNCAP ALA-877.  
 RX MEDLINE=92222955; PubMed=1562539;  
 RA Veldechoite J., Baerivoets C.A., Ris-Stalpers C., Kuiper G.G.,  
 Jenster G., Trapman J., Brinkmann A.O., Mulder E.;  
 RT "The androgen receptor in LNCap cells contains a mutation in the  
 ligand binding domain which affects steroid binding characteristics  
 and response to antiandrogens.";  
 RL J. Steroid Biochem. Mol. Biol. 41:665-669(1992).  
 [21]  
 RN VARIANT MET-730.  
 RX MEDLINE=92335289; PubMed=1631125;  
 RA Neemark J.R., Hardy D.O., Tonb D.C., Carter B.S., Epstein J.L.,  
 Isaacs W.B., Brown T.R., Barrack E.R.;  
 RT "Androgen receptor gene mutations in human prostate cancer.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6319-6323(1992).

RN [22]  
 RP VARIANT CAIS VAL-754.  
 RX MEDLINE-93372806; PubMed-8103398;  
 RA Lobbaccaro J.-M., Lumbroso S., Ktari R., Dumas R., Sultan C.;  
 RT "An exonic point mutation creates a Meili site in the androgen  
 RT receptor gene of a family with complete androgen insensitivity  
 RT syndrome.";  
 RL Hum. Mol. Genet. 2:1041-1043(1993).  
 RN [23]  
 RP VARIANT CAIS ARG-807.  
 RX MEDLINE-94108430; PubMed-8281140;  
 RA Adeyemo O., Kallio P.J., Palvimo J.J., Kontula K., Jaenme O.A.;  
 RT "A single-base substitution in exon 6 of the androgen receptor gene  
 RT causing complete androgen insensitivity: the mutated receptor fails  
 RT to transactivate but binds to DNA in vitro.";  
 RL Hum. Mol. Genet. 2:1809-1812(1993).  
 RN [24]  
 RP VARIANT PAIS VAL-743.  
 RX MEDLINE-93315568; PubMed-8325932;  
 RA Nakao R., Yanase T., Sakai Y., Hagi M., Nawata H.;  
 RT "A single amino acid substitution (Gly743 -> Val) in the steroid-  
 RT binding domain of the human androgen receptor leads to Relfenstein

Query Match 24.4%; Score 61; DB 1; Length 919;  
 Best Local Similarity 48.3%; Pred. No. 13;  
 Matches 14; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 2 QDDPRTDCQCCRRCHQESGPRQOYCC 30  
 DB 61 QQQQQQQQQQQQQQQQQQQQETSPRQOQQQQ 89

RESULT 10

ANDR\_CANFA STANDARD; PRT; 907 AA.

AC 09T90;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).  
 GN AR OR NR3C4.

OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 RN [1]

SEQUENCE FROM N.A.

RT Lu B., Smock S.L., Castleberry T.A., Owen T.A.;  
 RT "Molecular cloning and functional characterization of the canine  
 RT androgen receptor";  
 RT Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC NR3 SUBFAMILY.

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CC -----

DR EMBL: AF197950; AAF18084.1; -

DR PROSITE: PS00031; NUCLEAR\_RECEPTOR; 1.

KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;

KM zinc-finger; steroid-binding. MODULATING (BY SIMILARITY).

FT DOMAIN 1 545  
 FT DNA\_BIND 547 612 C4-TYPE ZINC FINGERS (TWO).

FT ZN\_FING 547 567 C4-TYPE.  
 FT ZN\_FING 563 607 C4-TYPE.  
 FT DOMAIN 678 707 LIGAND-BINDING.  
 FT DOMAIN 55 64 POLY-GLN.  
 FT DOMAIN 70 76 POLY-GLN.  
 FT DOMAIN 131 134 POLY-GLN.  
 FT DOMAIN 202 202 POLY-GLN.  
 FT DOMAIN 329 332 POLY-SER.  
 FT DOMAIN 375 384 POLY-PRO.  
 FT DOMAIN 399 405 POLY-ALA.  
 SQ SEQUENCE 907 AA; 98726 MW; C6619F78DD2338AF CRC64;

Query Match 24.0%; Score 60; DB 1; Length 907;  
 Best Local Similarity 48.1%; Pred. No. 16;  
 Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 5 PQTDCQCCRRCHQESGPRQOYCC 31  
 DB 50 PGANHQQQQQQQQQQQQQQQQQQQETSPRQOQQQQ 76

RESULT 11

ANDR\_PANTR STANDARD; PRT; 911 AA.

AC 09T775;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).  
 GN AR OR NR3C4.

OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 RN [1]

SEQUENCE FROM N.A.  
 MEDLINE-98404153; PubMed-9732460;  
 RA Choong C.S., Kempainen J.A., Wilson E.M.;

RT "Evolution of the primate androgen receptor: a structural basis for  
 RT disease.";  
 RT J. Mol. Evol. 47:334-342(1998).

CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC NR3 SUBFAMILY.

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CC -----

DR EMBL: U94177; AAC73048.1; -

DR HSSP: P06536; IRGD.

DR INTERPRO: IPR000536; -

DR INTERPRO: IPR001103; -

DR INTERPRO: IPR001628; -

DR PFAM: PF00104; hormone\_rec; 1.

DR PFAM: PF00105; zf-C4; 1.

DR PRINTS: PR00047; STROIDFINGER.

DR PRINTS: PR00521; ANDROGENR.

DR PROSITE: PS00031; NUCLEAR\_RECEPTOR; 1.

KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;

KM zinc-finger; steroid-binding. MODULATING (BY SIMILARITY).

FT DOMAIN 1 549  
 FT DNA\_BIND 551 616 C4-TYPE ZINC FINGERS (TWO).



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FT DISULFD 263 272 BY SIMILARITY.
FT DISULFD 279 292 BY SIMILARITY.
FT DISULFD 286 301 BY SIMILARITY.
FT DISULFD 303 312 BY SIMILARITY.
FT DISULFD 319 330 BY SIMILARITY.
FT DISULFD 324 339 BY SIMILARITY.
FT DISULFD 341 350 BY SIMILARITY.
FT DISULFD 356 367 BY SIMILARITY.
FT DISULFD 361 378 BY SIMILARITY.
FT DISULFD 380 389 BY SIMILARITY.
FT DISULFD 396 409 BY SIMILARITY.
FT DISULFD 403 418 BY SIMILARITY.
FT DISULFD 420 429 BY SIMILARITY.
FT DISULFD 436 447 BY SIMILARITY.
FT DISULFD 441 456 BY SIMILARITY.
FT DISULFD 458 467 BY SIMILARITY.
FT DISULFD 474 485 BY SIMILARITY.
FT DISULFD 479 494 BY SIMILARITY.
FT DISULFD 496 505 BY SIMILARITY.
FT DISULFD 512 523 BY SIMILARITY.
FT DISULFD 517 532 BY SIMILARITY.
FT DISULFD 534 543 BY SIMILARITY.
FT DISULFD 550 560 BY SIMILARITY.
FT DISULFD 555 569 BY SIMILARITY.
FT DISULFD 571 580 BY SIMILARITY.
FT DISULFD 587 598 BY SIMILARITY.
FT DISULFD 592 607 BY SIMILARITY.
FT DISULFD 609 618 BY SIMILARITY.
FT DISULFD 625 635 BY SIMILARITY.
FT DISULFD 630 644 BY SIMILARITY.
FT DISULFD 646 655 BY SIMILARITY.
FT DISULFD 662 673 BY SIMILARITY.
FT DISULFD 667 682 BY SIMILARITY.
FT DISULFD 684 693 BY SIMILARITY.
FT DISULFD 700 710 BY SIMILARITY.
FT DISULFD 705 719 BY SIMILARITY.
FT DISULFD 721 730 BY SIMILARITY.
FT DISULFD 739 750 BY SIMILARITY.
FT DISULFD 744 759 BY SIMILARITY.
FT DISULFD 761 770 BY SIMILARITY.
FT DISULFD 776 787 BY SIMILARITY.
FT DISULFD 781 797 BY SIMILARITY.
FT DISULFD 799 808 BY SIMILARITY.
FT DISULFD 815 827 BY SIMILARITY.
FT DISULFD 821 836 BY SIMILARITY.
FT DISULFD 838 847 BY SIMILARITY.
FT DISULFD 854 865 BY SIMILARITY.
FT DISULFD 859 874 BY SIMILARITY.
FT DISULFD 876 885 BY SIMILARITY.
FT DISULFD 892 902 BY SIMILARITY.
FT DISULFD 897 911 BY SIMILARITY.
FT DISULFD 913 922 BY SIMILARITY.
FT DISULFD 929 940 BY SIMILARITY.
FT DISULFD 934 949 BY SIMILARITY.
FT DISULFD 951 960 BY SIMILARITY.
FT DISULFD 967 978 BY SIMILARITY.
FT DISULFD 972 987 BY SIMILARITY.
FT DISULFD 989 998 BY SIMILARITY.
FT DISULFD 1005 1016 BY SIMILARITY.
FT DISULFD 1010 1023 BY SIMILARITY.
FT DISULFD 1025 1034 BY SIMILARITY.
FT DISULFD 1041 1062 BY SIMILARITY.
FT DISULFD 1056 1071 BY SIMILARITY.
FT DISULFD 1073 1082 BY SIMILARITY.
FT DISULFD 1089 1100 BY SIMILARITY.
FT DISULFD 1094 1109 BY SIMILARITY.
FT DISULFD 1111 1120 BY SIMILARITY.
FT DISULFD 1127 1138 BY SIMILARITY.
FT DISULFD 1132 1147 BY SIMILARITY.
FT DISULFD 1149 1158 BY SIMILARITY.
FT DISULFD 1165 1183 BY SIMILARITY.
FT DISULFD 1177 1192 BY SIMILARITY.
FT DISULFD 1194 1203 BY SIMILARITY.

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FT DISULFD 1210 1223 BY SIMILARITY.
FT DISULFD 1215 1233 BY SIMILARITY.
FT DISULFD 1235 1244 BY SIMILARITY.

Query Match
Best Local Similarity 23.6%; Score 59; DB 1; Length 2318;
Matches 19; Conservative 5; Mismatches 17; Indels 32; Gaps 4;

OY 1 NODDPTDQ--QCOR-----RC-----RQESGPRQOYC----- 29
Db 1421 NVDDPWRGCEALQCRFLFNNSRCDPACSSPACLYNPDCTSGGRDTCNPYEKICADHF 1480
OY 30 -ORCKEICEEBE 41
Db 1481 ADGRCDQCGNTEE 1493

RESULT 13.
NRH3_MOUSE STANDARD; PRT; 445 AA.
ID NRH3_MOUSE
AC Q920Y9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE OXYSTEROLS RECEPTOR LXR-ALPHA (LIVER X RECEPTOR ALPHA) (NUCLEAR ORPHAN
GN NRH3 OR LXRA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Chen Y.E., Horiuchi M., Dzau V.J.;
RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: ORPHAN RECEPTOR. INTERACTION OF LXR ALPHA WITH RXR
CC SHIFTS RXR FROM ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN
CC ACTIVE LIGAND-BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES
CC THROUGH TARGET GENES DEFINED BY LXRES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NRI SUBFAMILY.
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CC -----
CC EMBL; AF085745; AAD16050.1; -.
CC HSSP; P20393; 1A6Y.
CC INTERPRO: IPR000536; -.
CC INTERPRO: IPR01628; -.
CC PFAM; PF00104; hormone_rec; 1.
CC PFAM; PF00105; zf-C4; 1.
CC PRINTS; PR00047; STROIDEFINGER.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger.
FT DNA_BIND 96 161 C4-TYPE ZINC FINGERS (TWO).
FT ZN_FING 96 116 C4-TYPE.
FT ZN_FING 132 156 C4-TYPE.
SQ SEQUENCE 445 AA; 50417 MW; 1A426F38D935731 CRC64;

Query Match
Best Local Similarity 23.2%; Score 58; DB 1; Length 445;
Matches 16; Conservative 9; Mismatches 5; Indels 10; Gaps 4;

OY 9 COOCO-RRCROESGPRQOYC-----ORCKEICEEBE 42
Db 148 COECLRKCRQ--AGNREE--CVLSEEOIRLKLKROEBE 183

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RESULT 14
NRH3_HUMAN STANDARD; PRT; 447 AA.
ID 013133;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE OXYSTEROLS RECEPTOR LXR-ALPHA (LIVER X RECEPTOR ALPHA) (NUCLEAR ORPHAN
DE RECEPTOR LXR-ALPHA).
GN NRH3 OR LXR-ALPHA.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95262897; PubMed-7744246;
RA Willy P.J., Umehono K., Ong E.S., Evans R.M., Heyman R.A.,
RA Mangelsdorf D.J.;
RT "LXR, a nuclear receptor that defines a distinct retinoid response
RT pathway."
RL Genes Dev. 9:1033-1045(1995).
CC -!- FUNCTION: ORPHAN RECEPTOR. INTERACTION OF LXR ALPHA WITH RXR
CC SHIFTS RXR FROM ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN
CC ACTIVE LIGAND-BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES
CC THROUGH TARGET GENES DEFINED BY LXRES.
CC -!- SUBUNIT: INTERACTS WITH RXR..
CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -!- INDUCTION: BY 9-CIS RETINOIC ACID (9CRA).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NRI SUBFAMILY.
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CC
CC EMBL: U22662; AAA5856.1; -.
CC HSSP: P20393; IABY.
CC DR 602423; -.
CC DR INTERPRO: IPR000536; -.
CC DR INTERPRO: IPR001628; -.
CC DR PFAM: PF00104; hormone_rec; 1.
CC DR PFAM: PF00105; zf-C4; 1.
CC DR PRINTS: PRO0047; STROIDFINGER.
CC DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
CC KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger.
FT DNA_BIND 98 163 C4-TYPE ZINC FINGERS (TWO).
FT ZN_FING 98 118 C4-TYPE.
FT ZN_FING 134 158 C4-TYPE.
SQ SEQUENCE 447 AA; 50480 MW; A227B233DB0F8C96 CRC64;

Query Match 23.2%; Score 58; DB 1; Length 447;
Best Local Similarity 40.0%; Pred. No. 15;
Matches 16; Conservative 9; Mismatches 5; Indels 10; Gaps 4;
OY 9 COOQO-RRCROESGPROOYC-----ORRCKEICEEER 42
DB 150 CQECRLKRCQ--AGMRE--CVLSEQIRLKLKROEE 185

RESULT 15
KAPC_DICDI STANDARD; PRT; 648 AA.
AC P34099;
DT 01-FEB-1994 (Rel. 28, Created)

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DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (EC 2.7.1.37).
GN PKAC OR PK2 OR PK3.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostellida; Dictyostelium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91323730; PubMed-1864510;
RA Buerki E., Anjard C., Scholder J.-C., Reymond C.D.;
RT "Isolation of two genes encoding putative protein kinases regulated
RT during Dictyostelium discoideum development."
RL Gene 102:57-65(1991).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE-93385090; PubMed-8373760;
RA Anjard C., Etchebhere L., Pinard S., Veron M., Reymond C.D.;
RT "An unusual catalytic subunit for the CAMP-dependent protein kinase
RT of Dictyostelium discoideum."
RL Biochemistry 32:9532-9538(1993).
RN [3]
RP CHARACTERIZATION.
RX STRAT-AX3;
RX MEDLINE-93066311; PubMed-1332055;
RA Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.;
RT "Dpk3, which plays essential roles during Dictyostelium development,
RT encodes the catalytic subunit of CAMP-dependent protein kinase."
RL Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705(1992).
CC -!- FUNCTION: ESSENTIAL FOR DIFFERENTIATION AND FRUIT MORPHOGENESIS.
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
CC -!- SUBUNIT: IN DICTYOSTELIUM THE HOLOENZYME IS A DIMER COMPOSED OF
CC A REGULATORY (R) AND A CATALYTIC (C) SUBUNIT. IN THE PRESENCE OF
CC CAMP IT DISSOCIATES INTO THE ACTIVE C SUBUNIT AND AN R MONOMER.
CC -!- DEVELOPMENTAL STAGE: CAMP ACTIVITY IS LOW IN VEGETATIVELY GROWING
CC AMOEBAE, INCREASES DURING DEVELOPMENT OF AGGREGATION AND REACHES
CC A MAXIMUM AT CULMINATION.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMP SUBFAMILY.
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CC
CC EMBL: M38703; -. NOT_ANNOTATED_CDS.
CC PIR: JQ1150; JQ1150.
CC DR HSSP: P05132; ZCPK.
CC DR DICTYDB: DB02030; PKAC.
CC DR INTERPRO: IPR000719; -.
CC DR INTERPRO: IPR000961; -.
CC DR INTERPRO: IPR002290; -.
CC DR PFAM: PF00069; pk_kinase; 1.
CC DR PFAM: PF00433; pk_kinase_C; 1.
CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC KW Transferase; Serine/threonine-protein kinase; ATP-binding; CAMP;
CC Phosphorylation.
FT DOMAIN 58 64 ASN-RICH.
FT DOMAIN 136 223 GLN-RICH.
FT DOMAIN 233 250 THR-RICH.
FT DOMAIN 336 590 PROTEIN KINASE.
FT NP_BIND 342 350 ATP (BY SIMILARITY).
FT BINDING 365 365 ATP (BY SIMILARITY).
FT ACT_SITE 459 459 BY SIMILARITY.
FT MOD_RES 490 490 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 648 AA; 74458 MW; D0F9B3A48C58D084 CRC64;

Query Match 23.2%; Score 58; DB 1; Length 648;

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